



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/726,148
Source: FWP
Date Processed by STIC: 12/17/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 101726,148

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use **space characters**, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



II

RAW SEQUENCE LISTING

DATE: 12/17/2003

PATENT APPLICATION: US/10/726,148

TIME: 10:25:26

Input Set : A:\2544us1N.seq.txt

Output Set: N:\CRF4\12112003\J726148.raw

3 <110> APPLICANT: YOSHIMURA, Koji
 4 HIKICHI, Yuichi
 5 NISHIMURA, Atsushi
 7 <120> TITLE OF INVENTION: Novel Protein and DNA Thereof
 9 <130> FILE REFERENCE: 2544 US1N
 > 10 <140> CURRENT APPLICATION NUMBER:
 > 11 <141> CURRENT FILING DATE: 2003-12-02
 13 <150> PRIOR APPLICATION NUMBER: US 09/786256
 14 <151> PRIOR FILING DATE: 2001-03-02
 16 <150> PRIOR APPLICATION NUMBER: PCT/JP99/04766
 17 <151> PRIOR FILING DATE: 1999-09-02
 19 <150> PRIOR APPLICATION NUMBER: JP 10-250115
 20 <151> PRIOR FILING DATE: 1998-09-03
 22 <160> NUMBER OF SEQ ID NOS: 32
 24 <170> SOFTWARE: PatentIn version 3.0
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 540
 28 <212> TYPE: PRT
 29 <213> ORGANISM: Homo sapiens
 31 <220> FEATURE:
 32 <221> NAME/KEY: PEPTIDE
 33 <222> LOCATION: (1)..(540)
 34 <223> OTHER INFORMATION: An isolated ADAM family protein
 37 <400> SEQUENCE: 1
 39 Met Leu Gln Gly Leu Leu Pro Val Ser Leu Leu Leu Ser Val Ala Val
 40 1 5 10 15
 42 Ser Ala Ile Lys Glu Leu Pro Gly Val Lys Lys Tyr Glu Val Val Tyr
 43 20 25 30
 45 Pro Ile Arg Leu His Pro Leu His Lys Arg Glu Ala Lys Glu Pro Glu
 46 35 40 45
 48 Gln Gln Glu Gln Phe Glu Thr Glu Leu Lys Tyr Lys Met Thr Ile Asn
 49 50 55 60
 51 Gly Lys Ile Ala Val Leu Tyr Leu Lys Lys Asn Lys Asn Leu Leu Ala
 52 65 70 75 80
 54 Pro Gly Tyr Thr Glu Thr Tyr Tyr Asn Ser Thr Gly Lys Glu Ile Thr
 55 85 90 95
 57 Thr Ser Pro Gln Ile Met Asp Asp Cys Tyr Tyr Gln Gly His Ile Leu
 58 100 105 110
 60 Asn Glu Lys Val Ser Asp Ala Ser Ile Ser Thr Cys Arg Gly Leu Arg
 61 115 120 125
 63 Gly Tyr Phe Ser Gln Gly Asp Gln Arg Tyr Phe Ile Glu Pro Leu Ser
 64 130 135 140
 66 Pro Ile His Arg Asp Gly Gln Glu His Ala Leu Phe Lys Tyr Asn Pro

Does Not Comply
 Corrected Database Number

p.5

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Input Set : A:\2544us1N.seq.txt

Output Set: N:\CRF4\12112003\J726148.raw

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67 145          150          155          160
69 Asp Glu Lys Asn Tyr Asp Ser Thr Cys Gly Met Asp Gly Val Leu Trp
70          165          170          175
72 Ala His Asp Leu Gln Gln Asn Ile Ala Leu Pro Ala Thr Lys Leu Val
73          180          185          190
75 Lys Leu Lys Asp Arg Lys Val Gln Glu His Glu Lys Tyr Ile Glu Tyr
76          195          200          205
78 Tyr Leu Val Leu Asp Asn Gly Glu Phe Lys Arg Tyr Asn Glu Asn Gln
79          210          215          220
81 Asp Glu Ile Arg Lys Arg Val Phe Glu Met Ala Asn Tyr Val Asn Met
82 225          230          235          240
84 Leu Tyr Lys Lys Leu Asn Thr His Val Ala Leu Val Gly Met Glu Ile
85          245          250          255
87 Trp Thr Asp Lys Asp Lys Ile Lys Ile Thr Pro Asn Ala Ser Phe Thr
88          260          265          270
90 Leu Glu Asn Phe Ser Lys Trp Arg Gly Ser Val Leu Ser Arg Arg Lys
91          275          280          285
93 Arg His Asp Ile Ala Gln Leu Ile Thr Ala Thr Glu Leu Ala Gly Thr
94          290          295          300
96 Thr Val Gly Leu Ala Phe Met Ser Thr Met Cys Ser Pro Tyr Ser Val
97 305          310          315          320
99 Gly Val Val Gln Asp His Ser Asp Asn Leu Leu Arg Val Ala Gly Thr
100          325          330          335
102 Met Ala His Glu Met Gly His Asn Phe Gly Met Phe His Asp Asp Tyr
103          340          345          350
105 Ser Cys Lys Cys Pro Ser Thr Ile Cys Val Met Asp Lys Ala Leu Ser
106          355          360          365
108 Phe Tyr Ile Pro Thr Asp Phe Ser Ser Cys Ser Arg Leu Ser Tyr Asp
109          370          375          380
111 Lys Phe Phe Glu Asp Lys Leu Ser Asn Cys Leu Phe Asn Ala Pro Leu
112 385          390          395          400
114 Pro Thr Asp Ile Ile Ser Thr Pro Ile Cys Gly Asn Gln Leu Val Glu
115          405          410          415
117 Met Gly Glu Asp Cys Asp Cys Gly Thr Ser Glu Glu Cys Thr Asn Ile
118          420          425          430
120 Cys Cys Asp Ala Lys Thr Cys Lys Ile Lys Ala Thr Phe Gln Cys Ala
121          435          440          445
123 Leu Gly Glu Cys Cys Glu Lys Cys Gln Phe Lys Lys Ala Gly Met Val
124          450          455          460
126 Cys Arg Pro Ala Lys Asp Glu Cys Asp Leu Pro Glu Met Cys Asn Gly
127 465          470          475          480
129 Lys Ser Gly Asn Cys Pro Asp Asp Arg Phe Gln Val Asn Gly Phe Pro
130          485          490          495
132 Cys His His Gly Lys Gly His Cys Leu Met Gly Thr Cys Pro Thr Leu
133          500          505          510
135 Gln Glu Gln Cys Thr Glu Leu Trp Gly Pro Gly Arg Arg Thr Asn Pro
136          515          520          525
138 Phe Pro Cys Ala Cys Ala Lys Glu Asn His Phe Arg
139          530          535          540

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Input Set : A:\2544us1N.seq.txt

Output Set: N:\CRF4\12112003\J726148.raw

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141 <210> SEQ ID NO: 2
142 <211> LENGTH: 96
143 <212> TYPE: PRT
144 <213> ORGANISM: Homo sapiens
146 <220> FEATURE:
147 <221> NAME/KEY: PEPTIDE
148 <222> LOCATION: (1)..(96)
149 <223> OTHER INFORMATION: Isolated fragment of Protein of Seq ID No.1 (aa 400-495)
152 <400> SEQUENCE: 2
154 Leu Pro Thr Asp Ile Ile Ser Thr Pro Ile Cys Gly Asn Gln Leu Val
155 1 5 10 15
157 Glu Met Gly Glu Asp Cys Asp Cys Gly Thr Ser Glu Glu Cys Thr Asn
158 20 25 30
160 Ile Cys Cys Asp Ala Lys Thr Cys Lys Ile Lys Ala Thr Phe Gln Cys
161 35 40 45
163 Ala Leu Gly Glu Cys Cys Glu Lys Cys Gln Phe Lys Lys Ala Gly Met
164 50 55 60
166 Val Cys Arg Pro Ala Lys Asp Glu Cys Asp Leu Pro Glu Met Cys Asn
167 65 70 75 80
169 Gly Lys Ser Gly Asn Cys Pro Asp Asp Arg Phe Gln Val Asn Gly Phe
170 85 90 95
172 <210> SEQ ID NO: 3
173 <211> LENGTH: 1620
174 <212> TYPE: DNA
175 <213> ORGANISM: Homo sapiens
177 <220> FEATURE:
178 <221> NAME/KEY: misc_feature
179 <222> LOCATION: (1)..(1620)
180 <223> OTHER INFORMATION: Isolated DNA encoding for the protein of SEQ ID NO.1
183 <400> SEQUENCE: 3
184 atgttgcaag gtctcttgcc agtcagtcct ctcctctctg ttgcagtaag tgctataaaa 60
186 gaactccctg ggggtaagaa gtatgaagtg gtttatccta taagacttca tccactgcat 120
188 aaaagagagg ccaaagagcc agagcaacag gaacaatttg aaactgaatt aaagtataaa 180
190 atgacaatta atggaaaaat tgcagtgctt tatttgaaaa aaaacaagaa cctccttgca 240
192 ccaggctaca cggaacata ttataattcc actggaaagg agatcaccac aagcccacaa 300
194 attatggatg attgttatta tcaaggacat attcttaatg aaaaggtttc tgacgctagc 360
196 atcagcacat gtaggggtct aaggggctac ttcagtcagg gggatcaaag atactttatt 420
198 gaacctttta gcccataca tcgggatgga caggagcatg cactcttcaa gtataaccct 480
200 gatgaaaaga attatgacag cacctgtggg atggatggtg tgttgtgggc ccacgatttg 540
202 cagcagaaca ttgccctacc tgccaccaa ctagtaaaat tgaaagacag gaaggttcag 600
204 gaacatgaga aatacataga atattatttg gtcctggata atggtgagtt taaaaggtag 660
206 aatgagaatc aagatgagat cagaaagagg gtatttgaga tggctaatta tgtcaacatg 720
208 ctttataaaa agctcaatac tcatgtggcc ttagttggta tggaaatctg gactgacaag 780
210 gataagataa agataacccc aaatgcaagc ttcaccttgg agaatttttc taaatggagg 840
212 gggagtgttc tctcaagaag aaagcgcat gatattgctc agttaatcac agcaacagaa 900
214 cttgctggaa cgactgtggg tcttgcatth atgtctacaa tgtgttctcc ttattctggt 960
216 ggcgttgttc aggaccacag cgataatctt cttagagttg cagggacaat ggcacatgaa 1020
218 atgggccaca actttggaat gtttcatgac gactattctt gcaagtgtcc ttctacaata 1080
220 tgtgtgatgg acaaaagcact gagcttctat ataccacag acttcagttc ctgcagccgt 1140

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Output Set: N:\CRF4\12112003\J726148.raw

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222 ctcagctatg acaagttttt tgaagataaa ttatcaaatt gcctctttta tgctccattg 1200
224 cctacagata tcatatccac tccaatttgt gggaaccagt tggtggaat gggagaggac 1260
226 tgtgattgtg ggacatctga ggaatgtacc aatatttgcg gtgatgctaa gacatgtaaa 1320
228 atcaaagcaa cttttcaatg tgcattagga gaatgttgcg aaaaatgcc aatttaaaaag 1380
230 gctgggatgg tgtgcagacc agcaaaagat gagtgcgacc tgctgaaat gtgtaatggt 1440
232 aaatctggta attgtcctga tgatagattc caagtcaatg gcttccttg ccatcacggg 1500
234 aagggccact gcttgatggg gacatgcccc aactgcagg agcagtgcac agagctgtgg 1560
236 ggaccaggtg ggaggacaaa tcctttcccc tgtgcatgtg cgaaggaaaa tcatttcaga 1620
239 <210> SEQ ID NO: 4
240 <211> LENGTH: 288
241 <212> TYPE: DNA
242 <213> ORGANISM: Homo sapiens
244 <220> FEATURE:
245 <221> NAME/KEY: misc_feature
246 <222> LOCATION: (1)..(288)
247 <223> OTHER INFORMATION: Artificial DNA encoding for peptide of SEQ ID NO.2
250 <400> SEQUENCE: 4
251 ttgcctacag atatcatatc cactccaatt tgtgggaacc agttgggtgga aatgggagag 60
253 gactgtgatt gtgggacatc tgaggaatgt accaatattt gctgtgatgc taagacatgt 120
255 aaaatcaaag caacttttca atgtgcatta ggagaatgtt gtgaaaaatg ccaattttaa 180
257 aaggctggga tgggtgtgcag accagcaaaa gatgagtgcg acctgcctga aatgtgtaat 240
259 ggtaaactctg gtaattgtcc tgatgataga ttccaagtca atggcttc 288
262 <210> SEQ ID NO: 5
263 <211> LENGTH: 201
264 <212> TYPE: PRT
265 <213> ORGANISM: Homo sapiens
267 <220> FEATURE:
268 <221> NAME/KEY: PEPTIDE
269 <222> LOCATION: (1)..(201)
270 <223> OTHER INFORMATION: Isolated fragment of protein of SEQ ID NO.1 (aa 199-399)
273 <400> SEQUENCE: 5
275 Val Gln Glu His Glu Lys Tyr Ile Glu Tyr Tyr Leu Val Leu Asp Asn
276 1 5 10 15
278 Gly Glu Phe Lys Arg Tyr Asn Glu Asn Gln Asp Glu Ile Arg Lys Arg
279 20 25 30
281 Val Phe Glu Met Ala Asn Tyr Val Asn Met Leu Tyr Lys Lys Leu Asn
282 35 40 45
284 Thr His Val Ala Leu Val Gly Met Glu Ile Trp Thr Asp Lys Asp Lys
285 50 55 60
287 Ile Lys Ile Thr Pro Asn Ala Ser Phe Thr Leu Glu Asn Phe Ser Lys
288 65 70 75 80
290 Trp Arg Gly Ser Val Leu Ser Arg Arg Lys Arg His Asp Ile Ala Gln
291 85 90 95
293 Leu Ile Thr Ala Thr Glu Leu Ala Gly Thr Thr Val Gly Leu Ala Phe
294 100 105 110
296 Met Ser Thr Met Cys Ser Pro Tyr Ser Val Gly Val Val Gln Asp His
297 115 120 125
299 Ser Asp Asn Leu Leu Arg Val Ala Gly Thr Met Ala His Glu Met Gly
300 130 135 140

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Input Set : A:\2544us1N.seq.txt

Output Set: N:\CRF4\12112003\J726148.raw

302 His Asn Phe Gly Met Phe His Asp Asp Tyr Ser Cys Lys Cys Pro Ser
 303 145 150 155 160
 305 Thr Ile Cys Val Met Asp Lys Ala Leu Ser Phe Tyr Ile Pro Thr Asp
 306 165 170 175
 308 Phe Ser Ser Cys Ser Arg Leu Ser Tyr Asp Lys Phe Phe Glu Asp Lys
 309 180 185 190
 311 Leu Ser Asn Cys Leu Phe Asn Ala Pro
 312 195 200

314 <210> SEQ ID NO: 6

315 <211> LENGTH: 10

316 <212> TYPE: PRT

317 <213> ORGANISM: Homo sapiens

319 <220> FEATURE:

320 <221> NAME/KEY: PEPTIDE

321 <222> LOCATION: (1)..(10)

322 <223> OTHER INFORMATION: Isolated fragment of Protein of SEQ ID NO.1 (aa 428-437)

325 <400> SEQUENCE: 6

327 Glu Cys Thr Asn Ile Cys Cys Asp Ala Lys

328 1 5 10

330 <210> SEQ ID NO: 7

331 <211> LENGTH: 23

332 <212> TYPE: DNA

333 <213> ORGANISM: Artificial

335 <220> FEATURE:

336 <223> OTHER INFORMATION: Nucleic Acid primer

338 <220> FEATURE:

339 <221> NAME/KEY: misc_feature

340 <222> LOCATION: (6)..(6)

341 <223> OTHER INFORMATION: modified base

344 <400> SEQUENCE: 7

> 345 gtrgansmdk sdgarsartg tga

348 <210> SEQ ID NO: 8

349 <211> LENGTH: 26

350 <212> TYPE: DNA

351 <213> ORGANISM: Artificial

353 <220> FEATURE:

354 <223> OTHER INFORMATION: Nucleic Acid primer

356 <220> FEATURE:

357 <221> NAME/KEY: misc_feature

358 <222> LOCATION: (13)..(13)

359 <223> OTHER INFORMATION: modified base

362 <220> FEATURE:

363 <221> NAME/KEY: misc_feature

364 <222> LOCATION: (21)..(21)

365 <223> OTHER INFORMATION: modified base

368 <400> SEQUENCE: 8

> 369 ayytgwdbbrd dwncdkvdds ngggca

372 <210> SEQ ID NO: 9

373 <211> LENGTH: 28

what base(s) can "n" represent? see item 9
 on Error
 summary
 sheet

23

same error

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RAW SEQUENCE LISTING ERROR SUMMARY
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TIME: 10:25:27

Input Set : A:\2544us1N.seq.txt
Output Set: N:\CRF4\12112003\J726148.raw

ase Note:

of n and/or Xaa have been detected in the Sequence Listing. Please review the
uence Listing to ensure that a corresponding explanation is presented in the <220>
<223> fields of each sequence which presents at least one n or Xaa.

#:7; N Pos. 6
#:8; N Pos. 13,21

alid <213> Response:

of "Artificial" only as "<213> Organism" response is incomplete,
1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

#:7,8,9,10,11,12,13,14,17,18,19,20,21,22,23,24,25,26,27,28

VERIFICATION SUMMARY

DATE: 12/17/2003

PATENT APPLICATION: US/10/726,148

TIME: 10:25:27

Input Set : A:\2544us1N.seq.txt

Output Set: N:\CRF4\12112003\J726148.raw

0 M:283 W: Missing Blank Line separator, <140> field identifier

1 M:271 C: Current Filing Date differs, Replaced Current Filing Date

45 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0

69 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0